

RAW SEQUENCE LISTING

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Application Serial Number: 10/589,851
Source: 1 FWO
Date Processed by STIC: 1/22/07

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RAW SEQUENCE LISTING

DATE: 01/22/2007

PATENT APPLICATION: US/10/589,851

TIME: 13:08:38

Input Set : E:\MEWB 013 00US SeqList.txt

Output Set: N:\CRF4\01222007\J589851.raw

5 <110> APPLICANT: Trowsdale, John
6 Eagle, Robert
7 Bacon, Louise
11 <120> TITLE OF INVENTION: Protein Ligands for NKG2D and UL16 Receptors and Uses
Thereof
15 <130> FILE REFERENCE: MEWB-013/00US
18 <140> CURRENT APPLICATION NUMBER: US 10/589,851
20 <141> CURRENT FILING DATE: 2006-08-17
23 <150> PRIOR APPLICATION NUMBER: PCT/GB2005/000572
25 <151> PRIOR FILING DATE: 2005-02-17
29 <150> PRIOR APPLICATION NUMBER: GB 0403491.4
31 <151> PRIOR FILING DATE: 2004-02-17
35 <160> NUMBER OF SEQ ID NOS: 16
39 <170> SOFTWARE: PatentIn version 3.1
43 <210> SEQ ID NO: 1
45 <211> LENGTH: 333
47 <212> TYPE: PRT
49 <213> ORGANISM: Homo sapiens
53 <400> SEQUENCE: 1
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59 Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser Leu
60 20 25 30
63 Cys Tyr Asp Ile Thr Val Ile Pro Lys Ile Arg Pro Gly Pro Arg Trp
64 35 40 45
67 Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr Asp
68 50 55 60
71 Cys Gly Ser Lys Arg Val Thr Pro Val Ser Pro Leu Gly Lys Lys Leu
72 65 70 75 80
75 Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu Val
76 85 90 95
79 Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn Tyr
80 100 105 110
83 Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu Gln
84 115 120 125
87 Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Pro Ser Phe Asp Gly
88 130 135 140
91 Gln Ile Phe Leu Leu Phe Asp Ser Gln Asn Arg Met Trp Thr Thr Thr
92 145 150 155 160
95 His Pro Gly Pro Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Asp
96 165 170 175
99 Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly Trp
100 180 185 190
103 Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala

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107 Gly Ala Pro Pro Thr Met Phe Ser Gly Thr Ala Gln Pro Arg Ala Thr
108          210          215          220
111 Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Met Cys Leu Leu Ile
112 225          230          235          240
115 Cys Ser Arg His Ser Leu Thr Gln Ser His Gly His His Pro Gln Ser
116          245          250          255
119 Leu Gln Pro Pro Pro His Pro Pro Leu Leu His Pro Thr Trp Leu Leu
120          260          265          270
123 Arg Arg Val Leu Trp Ser Asp Ser Tyr Gln Ile Ala Lys Arg Pro Leu
124          275          280          285
127 Ser Gly Gly His Val Thr Arg Val Thr Leu Pro Ile Ile Gly Asp Asp
128          290          295          300
131 Ser His Ser Leu Pro Cys Pro Leu Ala Leu Tyr Thr Ile Asn Asn Gly
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155 Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser Leu
156          20          25          30
159 Cys Tyr Asp Ile Thr Val Ile Pro Lys Ile Arg Pro Gly Pro Arg Trp
160          35          40          45
163 Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr Asp
164          50          55          60
167 Cys Gly Ser Lys Arg Val Thr Pro Val Ser Pro Leu Gly Lys Lys Leu
168 65          70          75          80
171 Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu Val
172          85          90          95
175 Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn Tyr
176          100          105          110
179 Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu Gln
180          115          120          125
183 Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Pro Ser Phe Asp Gly
184          130          135          140
187 Gln Ile Phe Leu Leu Phe Asp Ser Gln Asn Arg Met Trp Thr Thr Thr
188 145          150          155          160
191 His Pro Gly Pro Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Asp
192          165          170          175
195 Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly Trp
196          180          185          190
199 Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala
200          195          200          205
203 Gly Gly Thr Val

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220 actccccaat ggcagcggcc gccagccccc cggttccttt acgcctcccg cttctgctcc      120
222 tgctgtccag ctggtgcagg accgggctgg ccgacctca ctctctttgc tatgacatca      180
224 cgtcatccc taagttcaga cctggaccac ggtggtgtgc ggttcaaggc caggtggatg      240
226 aaaagacttt tcttactat gactgtggca gcaagacagt cacaccgtc agtcccctgg      300
228 ggaagaaact aaatgtcaca acggcctgga aagcacagaa ccagtagtg agagaggtgg      360
230 tggacatact tacagagcaa ctgcttgaca ttcagtgga gaattacata cccaaggaac      420
232 cctcaccct gcagggcagg atgtcttgat agcagaaagc cgaaggacac ggcagtggat      480
234 cttggcagct cagtttcgat ggacagatct tctcctctt tgactcagaa aacagaatgt      540
236 ggacaacggt tcatcctgga gccagaaaga tgaaagaaaa gtgggagaat gacaaggata      600
238 tgaccatgtc cttccattac atctcaatgg gagactgcac aggatggctt gaggacttct      660
240 tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accaccacc atgtcctcag      720
242 gcacagccca acccaggggc aaggccacca cctcctcct ttgctgcttc ctcatcatgt      780
244 gtctcctcat atgtcctcagg cacagtctga cccaaagcca tggccaccac cctcagtcct      840
246 tgcagcctcc tctcctcct cccctgcttc atcctacctg gctgctgaga agagtccttt      900
248 ggagtgcagc ctaccaaata gcgaagcgcc ccttgtctgg tggacacgtg actcgctga      960
250 ctttacctat cattggagac gactcacact ccttacctg cctccttgcc ttgtatacaa      1020
252 taaataacgg cgcagccagg tattcggagc cactcagggt tccatatctt gatggttccc      1080
254 tgggcccagc tgtcttttct tccgtcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1140
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261 <211> LENGTH: 939
263 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 4
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272 agctggtgca ggaccgggct ggccgaccct cactctcttt gctatgacat caccgtcatc      120
274 cctaagttca gacctggacc accgtggtgt gcggttcaag gccaggtgga tgaaaagact      180
276 tttcttcaat atgactgtgg cagcaagaca gtcacaccgc tcagtccctt ggggaagaaa      240
278 ctaaatgtca caacggcctg gaaagcacag aaccagtagc tgagagaggt ggtggacata      300
280 cttacagagc aactgcttga cattcagctg gagaattaca taccgaagga acccctcacc      360
282 ctgcaggcca ggatgtcttg tgagcagaaa gccgaaggac acggcagtg atcttggcag      420
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286 gttcatcctg gagccagaaa gatgaaagaa aagtgggaga atgacaagga tatgaccatg      540
288 tcttccatt acatctcaat gggagactgc acaggatggc ttgaggactt cttgatgggc      600
290 atggacagca ccctggagcc aagtgcagga ggcacagtct gacccaaagc catggccacc      660
292 accctcagtc cctgcagcct cctcctcatc ctcccctgct tcactctacc tggctgctga      720
294 ggagagtcc tggagtgac agctaccaa tagcgaagcg ccccttgtct ggtggacacg      780
296 tgactcgctg gactttacct atcattggag acgactcaca ctccttacc tgccctcttg      840
298 ccttgatatac aataaataac ggcgcagcca ggtattcgga gccactacag gtctccatat      900
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303 <210> SEQ ID NO: 5
305 <211> LENGTH: 246

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309 <213> ORGANISM: Homo sapiens
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323 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
324 35 40 45
327 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
328 50 55 60
331 Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
332 65 70 75 80
335 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
336 85 90 95
339 Val Val Asp Ile Leu Thr Glu Gln Leu Arg Asp Ile Gln Leu Glu Asn
340 100 105 110
343 Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
344 115 120 125
347 Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln Phe Ser Phe Asp
348 130 135 140
351 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Lys Arg Met Trp Thr Thr
352 145 150 155 160
355 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
356 165 170 175
359 Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly
360 180 185 190
363 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
364 195 200 205
367 Ala Gly Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala
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379 <210> SEQ ID NO: 6
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383 <212> TYPE: PRT
385 <213> ORGANISM: Homo sapiens
389 <400> SEQUENCE: 6
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395 Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
396 20 25 30
399 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
400 35 40 45
403 Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
404 50 55 60
407 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys

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411 Val Asn Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
412              85              90              95
415 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
416              100              105              110
419 Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Glu Met Phe Cys Gln His
420              115              120              125
423 Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Thr Ile Asn Gly
424              130              135              140
427 Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
428 145              150              155              160
431 Asn His Glu Ala Ser Lys Ile Lys Glu Thr Trp Lys Lys Asp Arg Gly
432              165              170              175
435 Leu Glu Lys Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
436              180              185              190
439 Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Glu Pro Thr Val
440              195              200              205
443 Ser Pro Val Asn Ala Ser Asp Ile His Trp Ser Ser Ser Ser Leu Pro
444 210              215              220
447 Asp Arg Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Val Leu Met Gly
448 225              230              235              240
451 Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Glu Trp Gln Ala Gly
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461 <211> LENGTH: 244
463 <212> TYPE: PRT
465 <213> ORGANISM: Homo sapiens
469 <400> SEQUENCE: 7
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476              20              25              30
479 Ser Leu Trp Tyr Asn Phe Thr Ile Ile His Leu Pro Arg His Gly Gln
480              35              40              45
483 Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln Lys Asn Phe Leu Ser
484 50              55              60
487 Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met Gly His Leu Glu Glu
488 65              70              75              80
491 Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln Leu Glu Met Leu Arg
492              85              90              95
495 Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala Asp Thr Glu Leu Glu
496              100              105              110
499 Asp Phe Thr Pro Ser Gly Pro Leu Thr Leu Gln Val Arg Met Ser Cys
500              115              120              125
503 Glu Cys Glu Ala Asp Gly Tyr Ile Arg Gly Ser Trp Gln Phe Ser Phe
504 130              135              140
507 Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg Lys Trp Thr

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VERIFICATION SUMMARY

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